

SEQUENCE LISTING

<110> Ole THRASTRUP et al.

<120> NOVEL FLUORESCENT PROTEINS

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<140> US 09/872,364

<141> 2001-06-01

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<170> PatentIn version 3.1

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 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
 15 20 25 30
 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 35 40 45
 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 50 55 60
 act ctc tct cat ggt gtt caa tgc ttt tct aga tac cca gat cat atg 241
 Thr Leu Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 65 70 75
 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag 289
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 80 85 90
 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct 337
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 95 100 105 110
 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 115 120 125
 ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa 433
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
 130 135 140
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 145 150 155
 aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga 529
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 160 165 170
 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat 577
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 175 180 185 190
 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc 625
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 195 200 205
 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag 673
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
 210 215 220
 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa 721
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 225 230 235
 taaatgtcca gacttccaat tgacactaaa gggatccgaa ttc 764

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 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
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 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser

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 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 35 40 45
 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 50 55 60
 act ctc tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg 241
 Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 65 70 75
 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag 289
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 80 85 90
 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct 337
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 95 100 105 110
 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385
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 115 120 125
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 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
 130 135 140
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 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
 145 150 155
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 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
 160 165 170
 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat 577
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 175 180 185 190
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 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 195 200 205

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 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
 210 215 220
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 35 40 45
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 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
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 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
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 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
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 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 35 40 45
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 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 50 55 60
 act ctc act tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg 241
 Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 65 70 75
 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag 289
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 80 85 90
 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct 337
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 95 100 105 110
 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 115 120 125
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 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
 130 135 140
 tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca aag 481
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
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 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
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 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat 577
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 175 180 185 190
 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc 625
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 195 200 205
 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag 673
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
 210 215 220
 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa 721
 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
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 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
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 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 115 120 125
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 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
 130 135 140
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 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
 145 150 155
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 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
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 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat 577
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 175 180 185 190
 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc 625
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 195 200 205
 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag 673
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 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
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 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
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<210> 23

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<213> Artificial Sequence

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<223> DNA sequence at the lacZ-promoter GFP fusion point

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